WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a nucleotide sequence that is greater than 80% identical to the nucleotide sequence GCCTCTGGGGAG (SEQ ID NO:1)

2. An isolated nucleic acid according to claim 1, wherein the nucleotide sequence is GCCTCTGGGGAG (SEQ ID NO:1).

3. An isolated nucleic acid according to claim 1, further comprising a nucleotide sequence that binds an Sp-1 transcription factor protein.

4. An isolated nucleic acid according to claim 3, wherein the nucleotide sequence is AGGTGGGACT (SEQ ID NO:2).

5. An isolated nucleic acid according to claim 1, further comprising an S1 nuclease sensitive site.

6. An isolated nucleic acid according to claim 5, wherein the S1 nuclease sensitive site is about 20 repeats of a sequence CCTT.

7. An isolated nucleic acid according to claim 3, further comprising an S1 nuclease sensitive site.

8. An isolated nucleic acid according to claim 7, wherein the S1 nuclease sensitive site is about 20 repeats of a sequence CCTT.

9. An isolated nucleic acid comprising a nucleotide sequence AGGTGGGACT (SEQ ID NO:2), which is 5' to a nucleotide sequence

GCCTCTGGGGAG (SEQ ID NO:1), which is 5' to about 20 repeats of a sequence CCTT.

10. An isolated nucleic acid according to claim 9, having a nucleotide sequence as depicted in Figure 6A (SEQ ID NO:3).

11. An isolated nucleic acid according to claim 9, wherein the nucleic acid sequences are approximately 7 kb genomic nucleic acid upstream of a $\beta_3$-AR transcription initiation site.

12. An isolated nucleic acid according to claim 5, further comprising a gene operatively associated with a promoter, wherein the gene and promoter are downstream of the *trans*-activator binding site and the S1 nuclease sensitive site.

13. An isolated nucleic acid according to claim 12, further comprising a nucleotide sequence that binds an Sp-1 transcription factor protein.

14. An isolated nucleic acid according to claim 9, further comprising a gene operatively associated with a promoter, wherein the gene and promoter are downstream of the AGGTGGGACT (SEQ ID NO:2) sequence, the GCCTCTGGGGAG (SEQ ID NO:1) sequence, and the repeats of the sequence CCTT.

15. An isolated nucleic acid according to claim 12, wherein the promoter is a herpes simplex virus thymidine kinase minimum promoter.

16. An isolated nucleic acid according to claim 12, wherein the promoter is a β3-adrenergic receptor (β3-AR) promoter.

17. An isolated nucleic acid according to claim 12, wherein the gene is a reporter gene.

18. An isolated nucleic acid according to claim 16, wherein the gene is a reporter gene.

19. A cell line containing the isolated nucleic acid according to claim 12.

20. A cell line containing the isolated nucleic acid according to claim 14.

21. A nucleic acid that hybridizes under conditions of high stringency with the nucleic acid according to claim 2.

22. A $\beta_3$-AR *trans*-activating factor polypeptide, wherein said polypeptide has the following characteristics:

(a) it binds specifically to the nucleic acid according to claim 2;

(b) it is expressed by brown adipose tissue cells;

(c) it is expressed at very low levels by cells isolated from the perirenal depot;

(d) an AP-2 binding nucleic acid does not compete with a nucleic acid comprising a nucleotide sequence GCCTCTGGGGAG (SEQ ID NO:1) for binding the polypeptide; and,

(e) when complexed to a nucleic acid comprising SEQ ID NO:1, it is not recognized by an antibody to AP-2.

23. A method of isolating a polypeptide that binds specifically to a nucleic acid having a nucleotide sequence GCCTCTGGGGAG (SEQ ID NO:1), which method comprises:

(a) contacting a composition suspected of containing the polypeptide with the nucleic acid under conditions that permit detection of binding of the polypeptide to the nucleic acid; and

(b) isolating the bound polypeptide.

24. A method according to claim 23, wherein the composition is a yeast hybrid assay system recombinantly engineered to express polypeptides from cells that express $\beta_3$-AR.

25. A method according to claim 24, wherein the cells are selected from the group consisting of human brown adipose tissue cells, human neuroblastoma cells, and HIB cells.

26. A method according to claim 23, wherein the composition is a nuclear extract from cells that endogenously express $\beta_3$-AR.

27. A method according to claim 26, wherein the cells are selected from the group consisting of human brown adipose tissue cells, human neuroblastoma cells, and HIB cells.

28. A method of screening for a compound that increases activity of a $\beta_3$-AR *trans*-activating factor in human cells, which method comprises:

(a) contacting cells capable of producing the $\beta_3$-AR *trans*-activating factor with a test compound; and

(b) detecting an increase in a level of activity of the $\beta_3$-AR *trans*-activating factor.

29. A method according to claim 28, wherein the increase in the level of activity of the β3-AR *trans*-activating factor is detected by detecting an increase in the level of expression of a reporter gene operatively associated with an isolated nucleic acid having a nucleotide sequence GCCTCTGGGGAG (SEQ ID NO:1) relative to a level of expression prior to contact with the test compound.

30. A method according to claim 29, wherein the increase in the level of activity of the β3-AR *trans*-activating factor is detected by detecting an increase in the amount of β3-AR *trans*-activating factor present in the cells after contacting them with the test compound relative to the amount present prior to contact with the test compound.

31. A method according to claim 28, wherein the cells do not endogenously express, or express at very low level, β3-AR.

32. A method according to claim 31, wherein the cells are selected from the group consisting of HeLa cells, CV-1cells, and WAT cells.

~~33~~. A method of screening for a compound that inhibits activity of a $\beta_3$-AR *trans*-activating factor in human cells, which method comprises:

(a) contacting cells capable of producing the $\beta_3$-AR *trans*-activating factor with a test compound; and

(b) detecting a decrease in a level of activity of the $\beta_3$-AR *trans*-activating factor.

34. A method according to claim 33, wherein the decrease in the level of activity of the $\beta_3$-AR *trans*-activating factor is detected by detecting a decrease in the level of expression of a reporter gene operatively associated with an isolated nucleic acid

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having a nucleotide sequence GCCTCTGGGGAG (SEQ ID NO:1) relative to a level of expression prior to contact with the test compound.

35. A method according to claim 33, wherein the decrease in the level of activity of the $\beta_3$-AR *trans*-activating factor is detected by detecting a decrease in the amount of $\beta_3$-AR *trans*-activating factor present in the cells after contacting them with the test compound relative to the amount present prior to contact with the test compound.

36. A method according to claim 33, wherein the cells endogenously express $\beta_3$-AR.

37. A method according to claim 36, wherein the cells are selected from the group consisting of neuroblastoma and BAT cells.

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